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Sequence Listing could not be accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=20; hr=14; min=22; sec=45; ms=727; ]

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Reviewer Comments:

<110> APPLICANT: SmithKline Beecham Biologicals  
Ruelle, Jean-Louis

<120> TITLE OF INVENTION: BASB029 Polynucleotides and Polypeptides  
from Neisseria Meningitidis

<130> FILE REFERENCE: BM45321

<140> CURRENT APPLICATION NUMBER: 09700293

<141> CURRENT FILING DATE: 2000-11-13

<150> PRIOR APPLICATION NUMBER: PCT/EP99/03255

<151> PRIOR FILING DATE: 1999-05-07

<150> PRIOR APPLICATION NUMBER: GB 9810276.7

<151> PRIOR FILING DATE: 1998-05-13

<160> NUMBER OF SEQ ID NOS: 6

<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO 1

<211> LENGTH: 1785

<212> TYPE: DNA

<213> ORGANISM: Bacteria

<400> SEQUENCE: 1

Per the above, please do not insert alpha numeric headings in the sequence. The above <213> response for sequence id# 1 is invalid, please insert genus/species response. Please correct the remaining sequences showing similar errors.

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Application No: 09700293 Version No: 1.0

**Input Set:**

**Output Set:**

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**Finished:** 2008-10-27 13:37:46.171  
**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 513 ms  
**Total Warnings:** 6  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 6  
**Actual SeqID Count:** 6

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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)

<110> APPLICANT: SmithKline Beecham Biologicals  
Ruelle, Jean-Louis  
<120> TITLE OF INVENTION: BASB029 Polynucleotides and Polypeptides  
from Neisseria Meningitidis  
<130> FILE REFERENCE: BM45321

<140> CURRENT APPLICATION NUMBER:09700293  
<141> CURRENT FILING DATE:2000-11-13  
<150> PRIOR APPLICATION NUMBER: PCT/EP99/03255  
<151> PRIOR FILING DATE: 1999-05-07  
<150> PRIOR APPLICATION NUMBER: GB 9810276.7  
<151> PRIOR FILING DATE: 1998-05-13  
<160> NUMBER OF SEQ ID NOS: 6  
<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO 1  
<211> LENGTH: 1785  
<212> TYPE: DNA  
<213> ORGANISM: Bacteria  
<400> SEQUENCE: 1

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acactgttgt ttgcaacggt tcaggcgagt actaccgatg acgacgattt atatttagaa	180
cccgtacaac gcactgctgt cgttgtgagc ttccgttccg ataaagaagg cacgggagaa	240
aaagaagttt cagaagattt aaattggggta gtatatttcg acaagaaaagg agtactaaca	300
gccggaacaaa tcaccctcaa agccggcgac aacctgaaaa tcaaaacaaaa caccatgaa	360
aacaccaatg ccagtagctt cacctactcg ctgaaaaaaag acctcacaga tctgaccagt	420
gttggaaactg aaaaattatc gtttagcgca aacagcaata aagtcaacat cacaagcgac	480
acccaaaggct tgaatttgcg gaaaaaaaacg gctgagacca acggcgacac cacggttcat	540
ctgaacggta tcggttcgac tttgaccgat acgctgtga ataccggagc gaccacaaac	600
gtAACCCAAACG acaacgttac cgatgacgag aaaaaacgtg cggcaagcgt taaagacgt	660
ttaaacgcag gctggacat taaaggcggtt aaacccggta caacagttc cgataacgtt	720
gatttctgtcc gcacttacga cacagtcgag ttcttgagcg cagatacgaa aacaacgact	780
gttaatgtgg aaagcaaaga caacggcaag agaaccgaag taaaatcg tgcgaagact	840
tctgttatca aagaaaaaga cggtaagttt gttactggta aagacaaagg cgagaatgt	900
tcttctacag acaaaggcga aggcttagt gactgcaaaag aagtgattga tgcagtaaac	960
aaggctgggtt ggagaatgaa aacaacaacc gctaattggtc aaacaggtca agctgacaag	1020
tttggaaaccg ttacatcagg cacaatgta acctttgcta gtggtaaagg tacaactcg	1080
actgtaaatgtt aagatgatca aggcaacatc actgttatgt atgtatgtaaa tgcggcgat	1140
gcccattaaacg tcaatcagct gcaaaacacgc ggttggattt tggattccaa agcggttgc	1200
ggttcttcgg gcaaaagtcat cagcggcaat gtttgcggca gcaaggggaaa gatggatgaa	1260
accgtcaaca ttaatgccgg caacaacatc gagattaccc gcaacggcaa aaatatcgac	1320
atcgccactt cgtatgaccc gcaattttcc agcggttgcg tggcgccggg ggcggatcg	1380
cccaactttaa gctgtggatga cgagggcgcg ttgaatgtcg gcagcaagga tgccaacaaa	1440
cccgccgca ttaccaatgt cgccccgggc gttaaagagg gggatgttac aaacgtcgca	1500
caacttaaag gctgtggcgca aaacttgaac aaccacatcg acaatgtgga cggcaacgcg	1560
cgtgcgggca tcgccaaggc gattgcaacc gcaggtctgg ttcaaggcgta tctgcccggc	1620
aagagtatgtt gggcgatcg cggcgactt tatcgccgca aagccggta tgccatcg	1680
tactcaagca tttccgacgg cgaaaattgg attatcaaag gcacggctt cggcaattcg	1740
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<210> SEQ ID NO 2  
<211> LENGTH: 594  
<212> TYPE: PRT  
<213> ORGANISM: Bacteria  
<400> SEQUENCE: 2

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Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala  
20 25 30  
Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln  
35 40 45  
Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg  
50 55 60  
Thr Ala Val Val Leu Ser Phe Arg Ser Asp Lys Glu Gly Thr Gly Glu  
65 70 75 80  
Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys  
85 90 95  
Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu  
100 105 110  
Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr  
115 120 125  
Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu  
130 135 140  
Lys Leu Ser Phe Ser Ala Asn Ser Asn Lys Val Asn Ile Thr Ser Asp  
145 150 155 160  
Thr Lys Gly Leu Asn Phe Ala Lys Lys Thr Ala Glu Thr Asn Gly Asp  
165 170 175  
Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu  
180 185 190  
Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp  
195 200 205  
Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly  
210 215 220  
Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val  
225 230 235 240  
Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr  
245 250 255  
Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr  
260 265 270  
Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly  
275 280 285  
Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Asp Ser Ser Thr Asp  
290 295 300  
Lys Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn  
305 310 315 320  
Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly  
325 330 335  
Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe  
340 345 350  
Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly  
355 360 365  
Asn Ile Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val  
370 375 380  
Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala  
385 390 395 400  
Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly  
405 410 415  
Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile  
420 425 430  
Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln  
435 440 445  
Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser  
450 455 460

Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys  
 465 470 475 480  
 Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val  
 485 490 495  
 Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His  
 500 505 510  
 Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile  
 515 520 525  
 Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met  
 530 535 540  
 Ala Ile Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly  
 545 550 555 560  
 Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala  
 565 570 575  
 Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr  
 580 585 590  
 Gln Trp

<210> SEQ ID NO 3  
 <211> LENGTH: 1776  
 <212> TYPE: DNA  
 <213> ORGANISM: Bacteria  
 <400> SEQUENCE: 3

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 acactgttgt ttgcaacggt tcaggcaagt gctaacaatg aagagcaaga agaagagatta 180  
 tatttagacc ccgtacaacg cactgttgcc gtgttgatag tcaattccga taaaagaaggc 240  
 acgggagaaaa aagaaaaagt agaagaaaat tcagattggg cagtatattt caacgagaaaa 300  
 ggagtagctaa cagccagaga aatcaccctc aaagccggcg acaacctgaa aatcaaacaa 360  
 aacggcacaa acttcaccta ctcgctgaaa aaagacctca cagatctgac cagtgttgaa 420  
 actgaaaaat tatcgtagt cgcaaaccgc aataaaagtca acatcacaag cgacacacaaa 480  
 ggcttgaatt ttgcgaaaga aacggctggg acgaacggcg acaccacggt tcacctgaaac 540  
 ggtattggtt cgactttgac cgatacgctg ctgaataccg gagcggaccac aaacgtaacc 600  
 aacgacaacg ttaccgatga cgagaaaaaa cgtgcggcaa gcgttaaaga cgtattaaac 660  
 gcaggctgga acattaaagg cgttaaaccg ggtacaacag cttccgataa cgttgatttc 720  
 gtccgcactt acgacacagt cgagttctg agcgcagata cggaaaacaac gactgttaat 780  
 gtggaaagca aagacaacgg caagaaaaacc gaagttaaaa tcggtgcgaa gacttctgtt 840  
 attaaagaaaa aagacggtaa gttggtaact ggtaaaagaca aaggcgagaa tggttcttct 900  
 acagacgaag gcgaaggcgtt agtgactgca aaagaagtga ttgatgcagt aaacaaggct 960  
 ggttggagaa tgaaaacaac aaccgctaat ggtcaaacag gtcaagctga caagtttcaa 1020  
 accgttacat caggcacaaa tgtaacctt gctagtggtt aaggtaacaac tgcgactgta 1080  
 agtaaagatg atcaaggcaa catcactgtt atgtatgatg taaatgtcgg cgatgcccta 1140  
 aacgtcaatc agctgcaaaa cagcgggttgg aattttggatt ccaaaggcggt tgcaggttct 1200  
 tcgggcaaaag tcatcagcgg caatgtttcg ccgagcaagg gaaagatgga tgaaaaccgtc 1260  
 aacattaaatg cccgcaacaa catcgagatt acccgcaacg gtaaaaatat cgacatcgcc 1320  
 acttcgatga ccccgcaactt ttccagcgtt tcgctcggcg cggggggcgga tgcgcccact 1380  
 ttgagcgtgg atggggacgc attgaatgtc ggcagcaaga aggacaacaa acccgccgc 1440  
 attaccaatg tgcggccggg cgttaaagag ggggatgtt caaacgtcgc acaacttaaaa 1500  
 ggcgtggcgc aaaacttgaa caaccgcattc gacaatgtgg acggcaacgc gcgtgcggc 1560  
 atcgcccaag cgattgcaac cgcaggctg gttcaggcgt atttgcccgg caagagtatg 1620  
 atggcgatcg gcggcgccac ttatcgccgc gaagccgggtt acggccatcg ctactccagt 1680  
 atttccgacg gcggaaattg gattatcaaa ggcacggctt ccggcaattc gcgccggccat 1740  
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<210> SEQ ID NO 4  
 <211> LENGTH: 591  
 <212> TYPE: PRT

<213> ORGANISM: Bacteria

<400> SEQUENCE: 4

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20 25 30  
Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln  
35 40 45  
Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro  
50 55 60  
Val Gln Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly  
65 70 75 80  
Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr  
85 90 95  
Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala  
100 105 110  
Gly Asp Asn Leu Lys Ile Lys Gln Asn Gly Thr Asn Phe Thr Tyr Ser  
115 120 125  
Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu  
130 135 140  
Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys  
145 150 155 160  
Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr  
165 170 175  
Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn  
180 185 190  
Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu  
195 200 205  
Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn  
210 215 220  
Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe  
225 230 235 240  
Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr  
245 250 255  
Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val  
260 265 270  
Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu  
275 280 285  
Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly  
290 295 300  
Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala  
305 310 315 320  
Gly Trp Arg Met Lys Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala  
325 330 335  
Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser  
340 345 350  
Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile  
355 360 365  
Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln  
370 375 380  
Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser  
385 390 395 400  
Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met  
405 410 415  
Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg  
420 425 430  
Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser

435	440	445
Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp		
450	455	460
Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg		
465	470	475
Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val		
485	490	495
Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn		
500	505	510
Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala		
515	520	525
Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly		
530	535	540
Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser		
545	550	555
Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn		
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Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp		
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<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Oligonucleotide	
<400> SEQUENCE: 5	
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